AMENDMENTS TO THE CLAIMS

- 1. 20 (Canceled)
- 21. (Previously Presented) An isolated first viral nucleic acid or complement thereof, wherein
 - (a) the first viral nucleic acid consists of 17 to 24 nucleotides;
 - (b) a second viral nucleic acid consisting of 50 to 131 nucleotides comprises the first viral nucleic acid;
 - (c) the second viral nucleic acid is capable of forming a hairpin, wherein
 - (i) the hairpin comprises two stem segments and an intervening loop segment;
 - (ii) the two stem segments each consist of 19 to 71 nucleotides;
 - (iii) the loop segment consists of 3 to 19 nucleotides;
 - (iv) the first and second stem segment are at least 44.1% complementary; and
 - (v) one of the stem segments of the hairpin comprises the first viral nucleic acid,
 - (d) the first viral nucleic acid is capable of binding to a binding site of a mRNA; and
 - (e) the first viral nucleic acid is capable of inhibiting expression of a protein encoded by a mRNA, wherein the mRNA comprises the binding site.
- 22. (Previously Presented) The nucleic acid of claim 21, wherein the first viral nucleic acid is at least 72.7% complementary to the mRNA.
- 23. (Previously Presented) The nucleic acid of claim 21, wherein the untranslated region of the mRNA comprises the binding site.
- 24. (Previously Presented) The nucleic acid of claim 21, wherein the hairpin is characterized by a negative free energy of folding of at least -11.3 Kcal/mol.
- 25. (Previously Presented) The nucleic acid of claim 21, wherein the mRNA is transcribed from the genome of the host of the virus.
- 26. (Previously Presented) The nucleic acid of claim 21, wherein the first viral nucleic acid and the mRNA are in different parts of a genome.

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- 27. (Previously Presented) The nucleic acid of claim 21, wherein the viral nucleic acid is from a DNA virus.
- 28. (Previously Presented) The nucleic acid of claim 27, wherein the virus is selected from the group consisting of: human adenovirus, adeno-associated virus, B19 virus, human herpesvirus, human papillomavirus, molluscum contagiosum virus, ovine adenovirus, rat cytomegalovirus, vaccinia virus and variola virus.
- 29. (Previously Presented) The nucleic acid of claim 21, wherein the viral nucleic acid is from a RNA virus.
- 30. (Previously Presented) The nucleic acid of claim 29, wherein the virus is selected from the group consisting of: Barmah forest virus, Borna disease virus, bovine kobuvirus, Colorado tick fever virus, dengue virus, Eastern equine encephalitis virus, Encephalomyocarditis virus, equine rhinovirus, hepatitis virus, human astrovirus, human coronavirus, human echovirus, human enterovirus, human metapneumovirus, human parainfluenza virus, human respiratory syncytial virus, human rhinovirus, influenza virus, Japanese encephalitis virus, Marburg virus, measles virus, Murray valley encephalitis virus, Norwalk virus, poliovirus, respiratory syncytial virus, reston Ebola virus, rubella virus, salmon pancreas disease virus, SARS coronavirus, simian picornavirus 1, Sindbis virus, sleeping disease virus, tick-borne encephalitis virus, transmissible gastroenteritis virus, West Nile virus, Western equine encephalomyelitis virus, Yellow Fever virus and Zaire Ebola virus.
- 31. (Previously Presented) The nucleic acid of claim 29, wherein the viral nucleic acid is a retrovirus.
- 32. (Previously Presented) The nucleic acid of claim 31, wherein the virus is selected from the group consisting of: human immunodeficiency virus 1, human immunodeficiency virus 2, human T-lymphotropic virus 2 and simian immunodeficiency virus.
- 33. (Previously Presented) A probe comprising a nucleic acid according to any one of claims 21-32.
- 34. (Previously Presented) A vector comprising a nucleic acid according to any one of claims 21-32.
- 35. (Currently Amended) An isolated first viral nucleic acid or complement thereof, wherein

- (a) the first viral nucleic acid <u>consisting consists</u> of 50 to 131 nucleotides and comprises a second viral nucleic acid;
- (b) the second viral nucleic acid consists of 17 to 24 nucleotides;
- (c) the first viral nucleic acid is capable of forming a hairpin, wherein
 - (i) the hairpin comprises two stem segments and an intervening loop segment;
 - (ii) the two stem segments each consist of 19 to 71 nucleotides;
 - (iii)the loop segment consists of 3 to 19 nucleotides;
 - (iv)the first and second stem segment are at least 44.1% complementary; and
 - (v) one of the stem segments of the hairpin comprises the second viral nucleic acid,
 - (d) the second viral nucleic acid is capable of binding to a binding site of a mRNA; and
 - (e) the second viral nucleic acid is capable of inhibiting expression of a protein encoded by a mRNA, wherein the mRNA comprises the binding site.
- 36. (Previously Presented) The nucleic acid of claim 35, wherein the second viral nucleic acid is at least 72.7% complementary to the mRNA.
- 37. (Previously Presented) The nucleic acid of claim 35, wherein the untranslated region of the mRNA comprises the binding site.
- 38. (Previously Presented) The nucleic acid of claim 35, wherein the hairpin is characterized by a negative free energy of folding of at least -11.3 Kcal/mol.
- 39. (Previously Presented) The nucleic acid of claim 35, wherein the mRNA is transcribed from the genome of the host of the virus.
- 40. (Previously Presented) The nucleic acid of claim 35, wherein the second viral nucleic acid and the mRNA are in different parts of a genome.
- 41. (Previously Presented) The nucleic acid of claim 35, wherein the viral nucleic acid is from a DNA virus.
- 42. (Previously Presented) The nucleic acid of claim 41, wherein the virus is selected from the group consisting of: human adenovirus, adeno-associated virus, B19 virus, human herpesvirus, human papillomavirus, molluscum contagiosum virus, ovine adenovirus, rat cytomegalovirus, vaccinia virus and variola virus.

- 43. (Previously Presented) The nucleic acid of claim 35, wherein the viral nucleic acid is from a RNA virus.
- 44. (Previously Presented) The nucleic acid of claim 43, wherein the virus is selected from the group consisting of: Barmah forest virus, Borna disease virus, bovine kobuvirus, Colorado tick fever virus, dengue virus, Eastern equine encephalitis virus, Encephalomyocarditis virus, equine rhinovirus, hepatitis virus, human astrovirus, human coronavirus, human echovirus, human enterovirus, human metapneumovirus, human parainfluenza virus, human respiratory syncytial virus, human rhinovirus, influenza virus, Japanese encephalitis virus, Marburg virus, measles virus, Murray valley encephalitis virus, Norwalk virus, poliovirus, respiratory syncytial virus, reston Ebola virus, rubella virus, salmon pancreas disease virus, SARS coronavirus, simian picornavirus 1, Sindbis virus, sleeping disease virus, tick-borne encephalitis virus, transmissible gastroenteritis virus, West Nile virus, Western equine encephalomyelitis virus, Yellow Fever virus and Zaire Ebola virus.
- 45. (Previously Presented) The nucleic acid of claim 43, wherein the viral nucleic acid is a retrovirus.
- 46. (Previously Presented) The nucleic acid of claim 45, wherein the virus is selected from the group consisting of: human immunodeficiency virus 1, human immunodeficiency virus 2, human T-lymphotropic virus 2 and simian immunodeficiency virus.
- 47. (Previously Presented) A probe comprising a nucleic acid according to any one of claims 35-46.
- 48. (Previously Presented) A vector comprising a nucleic acid according to any one of claims 35-46.
- 49. (Previously Presented) An isolated nucleic acid wherein the nucleic acid is at least 72.7% identical to the nucleic acid of claim 21.
- 50. (New) The nucleic acid of claim 21, wherein the first viral nucleic acid comprises a sequence as set forth in any one of SEQ ID NOs: 1,557-3,353, or a complement thereof.
- 51. (New) The nucleic acid of claim 35, wherein the first viral nucleic acid comprises a sequence as set forth in any one of SEQ ID NOs: 1-1,556, or a complement thereof.

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